

SEQUENCE LISTING

<110> Asundi, Vinod  
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Zhang, Jie  
Zhou, Ping

<120> EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS

<130> 28110/36737

<150> US 09/620,312  
<151> 2000-07-19

<150> US 09/363,316  
<151> 1999-07-28

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gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt	96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe	
20 25 30	

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga	144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly	
35 40 45	

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc	192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser	
50 55 60	

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg	240
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr	
65 70 75 80	

tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt	288
Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys	
85 90 95	

09637860-101200

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Glu Asp Thr Glu  
100

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1 5 10 15

gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96  
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe  
20 25 30

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144  
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly  
35 40 45

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192  
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser  
50 55 60

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg 240  
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr  
65 70 75 80

tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt 288  
Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
85 90 95

gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc 336  
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu  
100 105 110

cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc 384  
Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala  
115 120 125

tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt 432  
Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe  
130 135 140

gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc 480  
Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile  
145 150 155 160

agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc 528  
Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser  
165 170 175

cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe 180 185 190	576
aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct Lys Cys Lys Cys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser 195 200 205	624
gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr 210 215 220	672
atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys 225 230 235 240	720
aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro 245 250 255	768
acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser 260 265 270	816
aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg Arg Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met 275 280 285	864
aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn 290 295 300	912
gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtc Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val 305 310 315 320	960
aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu 325 330 335	1008
act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser 340 345 350	1056
ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe 355 360 365	1104
gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala 370 375 380	1152
gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu 385 390 395 400	1200
ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp 405 410 415	1248
tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys 420 425 430	1296

aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu 435 440 445	1344
aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr 450 455 460	1392
aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu 465 470 475 480	1440
atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser 485 490 495	1488
ctt tta tct gtg gan nnc tgaatggtagtac tatctttata tttgactttg Leu Leu Ser Val Xaa Xaa 500	1536
tatgtcagtt ccctgggtttt tttgatattt catcatagga cctctggcat tttaaaatttt ctagctgaaa aattt	1596
1611	
 <p>&lt;210&gt; 3 &lt;211&gt; 100 &lt;212&gt; PRT &lt;213&gt; Homo sapiens</p> <p>&lt;400&gt; 3</p> <p>Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro 1 5 10 15 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe 20 25 30 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly 35 40 45 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser 50 55 60 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr 65 70 75 80 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys 85 90 95 Glu Asp Thr Glu 100</p> <p>&lt;210&gt; 4 &lt;211&gt; 537 &lt;212&gt; PRT &lt;213&gt; Homo sapiens</p> <p>&lt;220&gt; &lt;221&gt; VARIANT &lt;222&gt; (1)...(537) &lt;223&gt; Xaa = Any Amino Acid</p> <p>&lt;400&gt; 4</p> <p>Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro 1 5 10 15 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe 20 25 30 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly 35 40 45 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser 50 55 60</p>	

Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr  
 65 70 75 80  
 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
 85 90 95  
 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu  
 100 105 110  
 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala  
 115 120 125  
 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe  
 130 135 140  
 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile  
 145 150 155 160  
 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser  
 165 170 175  
 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe  
 180 185 190  
 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser  
 195 200 205  
 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr  
 210 215 220  
 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys  
 225 230 235 240  
 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro  
 245 250 255  
 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser  
 260 265 270  
 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met  
 275 280 285  
 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn  
 290 295 300  
  
 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val  
 305 310 315 320  
 Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu  
 325 330 335  
 Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser  
 340 345 350  
 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe  
 355 360 365  
 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala  
 370 375 380  
 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu  
 385 390 395 400  
 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp  
 405 410 415  
 Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys  
 420 425 430  
 Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu  
 435 440 445  
 Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr  
 450 455 460  
 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu  
 465 470 475 480  
 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser  
 485 490 495  
 Leu Leu Ser Val Asp Asp Xaa Met Val Leu Ser Leu Tyr Leu Thr Leu  
 500 505 510  
 Tyr Val Ser Ser Leu Val Phe Leu Ile Leu His His Arg Thr Ser Gly  
 515 520 525  
  
 Ile Leu Lys Leu Leu Ala Glu Lys Leu  
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<213> Homo sapiens

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ggaggcggcg gcttagctgc tacgggtcc ggccggcgcctcccgaggg gggctcagga
ggagaagga ggaccctgtc gaga atg cct ctg ccc tgg agc ctt gcg ctc
Met Pro Leu Pro Trp Ser Leu Ala Leu
1 5
ccg ctg ctg ctc ccc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt
Pro Leu Leu Leu Pro Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser
10 15 20 25
279
gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgc
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys
30 35 40
327
cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser
45 50 55
375
aag gga gtc tgc gaa gct aca tgc gaa cct gga tgc aag ttt ggt gag
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu
60 65 70
423
tgc gtc gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys
75 80 85
471
acc tgc agt caa gat gtc aat gag tgc gaa atg aaa ccc cgg cca tgc
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys
90 95 100 105
519
caa cac aga tgc gaa aat aca cac gga agc tac aag tgc ttt tgc ctc
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu
110 115 120
567
agt ggc cac atg ctc atg cca gat gct acg tgc tgc aac tct agg aca
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr
125 130 135
615
tgt gcc atg ata aac tgc cag tat agc tgc gaa gac aca gaa gaa ggg
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly
140 145 150
663
cca cag tgc ctg tgc cca tcc tca gga ctc cgc ctg gcc cca aat gga
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly
155 160 165
711
aga gac tgc cta gat att gat gaa tgc gct tct ggt aaa gtc atc tgc
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys
170 175 180 185
759
ccc tac aat cga aga tgc gtc aac aca ttt gga agc tac tac tgc aaa
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys
190 195 200
807

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09522893-40112000

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ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His 220 225 230	903
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln 235 240 245	951
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser 250 255 260 265	999
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys 270 275 280	1047
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys 285 290 295	1095
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu 300 305 310	1143
cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His 315 320 325	1191
gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat Gly Gly Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp 330 335 340 345	1239
gag aaa aga gaa gag aaa gcc ctg aag aat gac wta gag gag cga agc Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Xaa Glu Glu Arg Ser 350 355 360	1287
ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc Leu Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe 365 370 375	1335
ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His 380 385 390	1383
aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys 395 400 405	1431
gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp 410 415 420 425	1479
cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly 430 435 440	1527
cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Pro Asp Leu Gln 445 450 455	1575

ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac 1623  
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp  
460 465 470

aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg 1671  
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu  
475 480 485

gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa 1719  
Ala Trp Glu Lys Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys  
490 495 500 505

att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa 1767  
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu  
510 515 520

gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc 1815  
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val  
525 530 535

ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863  
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
540 545 550

tga atgttactat ctttatattt gactttgtat gtcagttccc tggtttttt 1916  
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gatattgsat cataggacct ctggcatttt aaaattacta agctgaaaaa ttgtaatgt 1976  
ccaaacagaaa ttattattgt aagatgcctt tmttgtataa gatatgc当地 tatttgcttt 2036  
aaatatcata tcactgtatc ttctcagtca tttctgaatc tttccacatt atattataaa 2096  
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atgagcttct ctctgcaaca tttctagaaaa atagahaaaa aagcacagag aaatgtttaa 2216  
ctgtttgact cttatgatag ttttgaaaa ctatgacatc aaagatagac ttttgccctaa 2276  
gtggcttagc tgggtcttcc atagccaaac ttgtatattt aaattctttg taataataat 2336  
atccaaatca tcaaaaaaaaaaaaaaaa 2365

<210> 6  
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<212> PRT  
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<220>  
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20 25 30  
Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala  
35 40 45  
Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr  
50 55 60  
Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys  
65 70 75 80  
Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn  
85 90 95  
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr  
100 105 110

His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
115 120 125  
Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln  
130 135 140  
Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser  
145 150 155 160  
Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp  
165 170 175  
Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val  
180 185 190  
Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu  
195 200 205  
Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr  
210 215 220  
Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln  
225 230 235 240  
Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu  
245 250 255  
Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala  
260 265 270  
Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn  
275 280 285  
Ser Met Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr  
290 295 300  
Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu  
305 310 315 320  
Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu  
325 330 335  
Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala  
340 345 350  
Leu Lys Asn Asp Xaa Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe  
355 360 365  
Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg  
370 375 380  
Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val  
385 390 395 400  
Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu  
405 410 415  
Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe  
420 425 430  
Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly Arg  
435 440 445  
Leu Lys Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu  
450 455 460  
Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val  
465 470 475 480  
Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser  
485 490 495  
Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr  
500 505 510  
Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys  
515 520 525  
Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys  
530 535 540

Pro Asp Ser Leu Leu Ser Val Asp Asp  
545 550

<210> 7  
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<212> PRT  
<213> Drosophila Melanogaster

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Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys Xaa Cys Pro Pro Gly Phe
      20          25          30
Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn
      35          40

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<210> 8  
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<213> *Homo sapiens*

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 Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys  
 1 5 10 15  
 Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys Cys Xaa Ser Gly Xaa Xaa  
 20 25 30  
 Gly Xaa Xaa Leu Xaa Cys Asp  
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<210> 9  
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<212> PRT  
<213> *Homo sapiens*

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<400> 9
Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Val Asn
      5          10          15
1
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
      20          25          30
2
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
      35          40          45
3
Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
      50          55          60
4
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
      65          70          75          80
5
Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys
      85          90          95
6
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys
      100         105         110
7
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu
      115         120         125
8
Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn
      130         135         140
9
Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
      145         150         155         160
10
Leu Arg Cys Ser

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<210> 10  
<211> 45  
<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(45)

<223> Xaa = Any Amino Acid

<400> 10

Val Xaa Glu Cys Xaa Ser Gly Xaa Gln Xaa Xaa Cys Xaa Ser Ser Xaa  
1 5 10 15

Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa Cys Arg Cys Arg Pro Gly  
20 25 30

Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa Xaa Xaa Asp  
35 40 45

<210> 11

<211> 58

<212> PRT

<213> Mammalian

<220>

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<222> (1)...(58)

<223> Xaa = Any Amino Acid

<400> 11

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His  
1 5 10 15

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn  
20 25 30

Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln  
35 40 45

Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg  
50 55

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Gene-specific PCR primer 10244-52

<400> 12

ctcatcctca agcccttctt t

21

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Gene-specific PCR primer 10244-51

<400> 13

ccatgagagt tcccgctct g

21

<210> 14

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Vector primer T7  
<400> 14  
gtaatacgac tcactatagg g 21  
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<211> 22  
<212> DNA  
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<220>  
<223> Vector primer SP6  
  
<400> 15 22  
attttaggtga cactatagaa gg  
  
<210> 16  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
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<223> Gene-specific PCR primer 10244-A  
  
<400> 16  
cccaggctga cgtgccatg c 21  
  
<210> 17  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Gene-specific PCR primer 10244-B  
  
<400> 17  
gcagcaggcc agtttagttc c 21  
  
<210> 18  
<211> 502  
<212> PRT  
<213> Homo sapiens  
  
<220>  
<221> VARIANT  
<222> (1)...(502)  
<223> Xaa = Any Amino Acid  
  
<400> 18  
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1 5 10 15  
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe  
20 25 30  
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly  
35 40 45  
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser  
50 55 60  
Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr  
65 70 75 80  
Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
85 90 95  
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu  
100 105 110

Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala  
115 120 125  
Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe  
130 135 140  
Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile  
145 150 155 160  
Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser  
165 170 175  
His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe  
180 185 190  
Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser  
195 200 205  
Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr  
210 215 220  
Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys  
225 230 235 240  
Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro  
245 250 255  
Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser  
260 265 270  
Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met  
275 280 285  
Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn  
290 295 300  
Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val  
305 310 315 320  
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu  
325 330 335  
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser  
340 345 350  
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe  
355 360 365  
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala  
370 375 380  
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu  
385 390 395 400  
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp  
405 410 415  
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys  
420 425 430  
Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu  
435 440 445  
Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr  
450 455 460  
Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu  
465 470 475 480  
Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser  
485 490 495  
Leu Leu Ser Val Xaa Xaa  
500

<210> 19  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 19

gtcatttctg aatcttcca c

<210> 20

<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 20  
gaaatgttgc agagagaagc tc 22  
  
<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 21  
ccagaacccca ccaggactcc 20  
  
<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: primer  
  
<400> 22  
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<210> 23  
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<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> CDS  
<222> (205)..(1863)  
  
<400> 23  
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tgcagggaca gcacccggta actgcgagtg gagcggagga cccgagcggc tgaggagaga 120  
ggaggcggcg gcttagctgc tacgggtcc ggccggcgcc ctcccgaggg gggctcagg 180  
ggaggaagga ggacccgtgc gaga atg cct ctg ccc tgg agc ctt gcg ctc 231  
Met Pro Leu Pro Trp Ser Leu Ala Leu  
1 5  
  
ccg ctg ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt 279  
Pro Leu Leu Leu Ser Trp Val Ala Gly Phe Gly Asn Ala Ala Ser  
10 15 20 25  
  
gca agg cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt 327  
Ala Arg His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys  
30 35 40  
  
cac tat gga act aaa ctg gcc tgc tac ggc tgg aga aga aac agc 375  
His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser  
45 50 55

095327860 - 1004300

aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag	423
Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu	
60 65 70	
tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa	471
Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys	
75 80 85	
acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc	519.
Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys	
90 95 100 105	
caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc	567
Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu	
110 115 120	
agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca	615
Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr	
125 130 135	
tgt gcc atg ata aac tgt cag tat agc tgt gaa gac aca gaa gaa ggg	663
Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly	
140 145 150	
cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga	711
Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly	
155 160 165	
aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt	759
Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys	
170 175 180 185	
ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa	807
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys	
190 195 200	
tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt	855
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys	
205 210 215	
ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat	903
Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His	
220 225 230	
gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag	951
Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln	
235 240 245	
gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct	999
Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser	
250 255 260 265	
gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag	1047
Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys	
270 275 280	
aag ttg ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa	1095
Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys	
285 290 295	
aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg	1143
Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu	
300 305 310	

cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat 1191  
Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His  
315 320 325

gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat 1239  
Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp  
330 335 340 345

gag aaa aga gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc 1287  
Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser  
350 355 360

ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc 1335  
Leu Arg Gly Asp Val Phe Pro Lys Val Asn Glu Ala Gly Glu Phe  
365 370 375

ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat 1383  
Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His  
380 385 390

aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt 1431  
Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys  
395 400 405

gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat 1479  
Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp  
410 415 420 425

cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt 1527  
Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly  
430 435 440

cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa 1575  
His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln  
445 450 455

ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac 1623  
Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp  
460 465 470

aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg 1671  
Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu  
475 480 485

gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa 1719  
Ala Trp Glu Lys Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys  
490 495 500 505

att cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa 1767  
Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu  
510 515 520

gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc 1815  
Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val  
525 530 535

ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac 1863  
Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
540 545 550

tgaatgttac tatctttata tttgactttg tatgtcagtt ccctggtttt tttgatattg 1923

satcatagga cctctggcat tttaaaatta ctaagctgaa aaattgtaat gtaccaacag 1983

aaattattat tgtaagatgc cttttttgtta taagatatgc caatattgc tttaaatatc 2043  
atatacactgt atcttctcag tcatttctga atctttccac attatattat aaaatatgga 2103  
aatgtcaggt ttatctcccc tcctcagttat atctgatttg tataagtaag ttgatgagct 2163  
tctctctgca acatttctag aaaatagaha aaaaagcaca gagaaatgtt taactgtttg 2223  
actcttatga tagttttgg aaactatgac atcaaagata gactttgcc taagtggctt 2283  
agctgggtct ttcatagcca aacttgtata tttaaattct ttgtaataat aatatccaaa 2343  
tcatcaaaaaa aaaaaaaaaa aa 2365

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<211> 553  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (1)...(553)

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Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His Gly Leu Leu  
20 25 30  
Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu Ala  
35 40 45  
Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr  
50 55 60  
Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys  
65 70 75 80  
Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn  
85 90 95  
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr  
100 105 110  
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
115 120 125  
Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln  
130 135 140  
Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser  
145 150 155 160  
Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp  
165 170 175  
Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val  
180 185 190

Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu  
195 200 205

Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr  
210 215 220

Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln  
225 230 235 240

Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu  
245 250 255

Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala  
260 265 270

Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn  
275 280 285

Ser Met Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr  
290 295 300

Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu  
305 310 315 320

Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu  
325 330 335

Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala  
340 345 350

Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe  
355 360 365

Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg  
370 375 380

Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val  
385 390 395 400

Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu  
405 410 415

Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe  
420 425 430

Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly Arg  
435 440 445

Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu  
450 455 460

Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val  
465 470 475 480

Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser  
485 490 495

Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr  
500 505 510

Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys  
515 520 525

09687860-1004300

Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys  
530 535 540

Pro Asp Ser Leu Leu Ser Val Asp Asp  
545 550

<210> 25  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 25  
ccctggcatg ggagaagacc ac 22

<210> 26  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 26  
gtgatatgtat atttaaagca aatattggca 30

<210> 27  
<211> 2360  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (190) .. (1869)

<220>  
<221> misc\_feature  
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<223> n = a,t,c or g

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ctcaactatacg ggctcgagcg gcccggccgg caggtgagga gagaggaggc ggccggcttag 120

ctgctacggg gtccggggccg gcgcctcccc gaggggggct caggaggagg aaggaggacc 180

cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228  
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu  
1 5 10

tcc tgg gtg qca ggt ggt ttc ggg aac gcg gcc agt gca agg ggt tct 276  
Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser  
14 19 24 29

0105327860-2012000

cat cat cat cat cat cac ggg ttg tta gca tcg gca cgt cag cct ggg	324
His His His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly	
30 35 40 45	
gtc tgt cac tat gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga	372
Val Cys His Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg	
46 51 56 61	
aac agc aag gga gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt	420
Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe	
62 67 72 77	
ggg gag tgc gtg gga cca aac aaa tgc aga tgc ttt cca gga tac acc	468
Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr	
78 83 88 93	
ggg aaa acc tgc agt caa gat gtg aat gag tgt gga atg aaa ccc cgg	516
Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg	
94 99 104 109	
cca tgc caa cac aga tgt gtg aat aca cac gga agc tac aag tgc ttt	564
Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe	
110 115 120 125	
tgc ctc agt ggc cac atg ctc atg cca gat gct acg tgt gtg aac tct	612
Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser	
126 131 136 141	
agg aca tgt gcc atg ata aac tgt cag tac agc tgt gaa gac aca gaa	660
Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu	
142 147 152 157	
gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca	708
Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro	
158 163 168 173	
aat gga aga gac tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc	756
Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val	
174 179 184 189	
atc tgt ccc tac aat cga aga tgt gtg aac aca ttt gga agc tac tac	804
Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr	
190 195 200 205	
tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc agt gga cga tat	852
Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr	
206 211 216 221	
gac tgt ata gat ata aat gaa tgt act atg gat agc cat acg tgc agc	900
Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser	
222 227 232 237	
cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc	948
His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys	
238 243 248 253	
aag cag gga tat aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa	996
Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu	
254 259 264 269	
aat tct gtg aag gaa gtc ctc aga gca cct ggt acc atc aaa gac aga	1044
Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg	
270 275 280 285	

atc aag aag ttg ctt gct cac aaa aac agt atg aaa aag aag gca aaa 1092  
Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys  
286 291 296 301

att aaa aat gtt acc cca gaa ccc acc agg act cct acc cct aag gtg 1140  
Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val  
302 307 312 317

aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac 1188  
Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn  
318 323 328 333

tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt 1236  
Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu  
334 339 344 349

gag gat gag aaa aga gaa gag aaa gcc ctg aag aat gac ata gag gag 1284  
Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu  
350 355 360 365

cga agc ctg cga gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt 1332  
Arg Ser Leu Arg Gly Asp Val Phe Pro Lys Val Asn Glu Ala Gly  
366 371 376 381

gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta act tcc aaa ctg 1380  
Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu  
382 387 392 397

gaa cat aaa gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg 1428  
Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly  
398 403 408 413

atc tgt gac tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct 1476  
Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro  
414 419 424 429

gct gat cga gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg 1524  
Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu  
430 435 440 445

gca ggt cac aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac 1572  
Ala Gly His Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Pro Asp  
446 451 456 461

ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc 1620  
Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala  
462 467 472 477

gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat 1668  
Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn  
478 483 488 493

gcc ctg gca tgg gag aag acc acg agt gag gat gaa aag tgg aag aca 1716  
Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr  
494 499 504 509

ggg aaa att cag ttg tat caa gga act gat gct acc aaa agc atc att 1764  
Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile  
510 515 520 525

ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat 1812  
Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp  
526 531 536 541

ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg	1860
Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val	
542 547 552 557	
gat gac tga atgttac tatcttata tttgactttg tatgtcagtt ccctggttt	1916
Asp Asp *	
558	
tttgatattg catcatagga cctctggcat tttagaatta ctagctgaaa aattgtaatg	1976
taccaacaga aatattattg taagatgcct ttcttgata agatatgcca atatttgctt	2036
taaatatcat atcaactgtat cttctcagtc atttctgaat ctttccacat tatattataa	2096
aatatggaaa tgcagttt tctccctcc tcagtatatc tgatttgtat aagtaagttg	2156
atgagcttct ctctacaaca tttctagaaa atagaaaaaa aagcacagag aaatgttaa	2216
ctgtttgact cttatgatac ttcttgaaa ctatgacatc aaagatagac ttttgcctaa	2276
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atccaaatca tcaaaaaaaaaaaa	2360

<210> 28  
<211> 559  
<212> PRT  
<213> Homo sapiens

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Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg Gly Ser His His His	
20 25 30	
His His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His	
35 40 45	
Tyr Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys	
50 55 60	
Gly Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys	
65 70 75 80	
Val Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr	
85 90 95	
Cys Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln	
100 105 110	
His Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser	
115 120 125	
Gly His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys	
130 135 140	
Ala Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro	
145 150 155 160	
Gln Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg	
165 170 175	

Asp Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro  
180 185 190

Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys  
195 200 205

His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile  
210 215 220

Asp Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala  
225 230 235 240

Asn Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly  
245 250 255

Tyr Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val  
260 265 270

Lys Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys  
275 280 285

Leu Leu Ala His Lys Asn Ser Met Lys Lys Lys Ala Lys Ile Lys Asn  
290 295 300

Val Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln  
305 310 315 320

Pro Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly  
325 330 335

Gly Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu  
340 345 350

Lys Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu  
355 360 365

Arg Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly  
370 375 380

Leu Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys  
385 390 395 400

Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp  
405 410 415

Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg  
420 425 430

Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His  
435 440 445

Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro  
450 455 460

Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys  
465 470 475 480

Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala  
485 490 495

Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile  
500 505 510

Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala  
515 520 525

Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu  
530 535 540

Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
545 550 555

<210> 29  
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<212> DNA  
<213> Homo sapiens

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<222> (190) .. (1854)

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<222> (1) .. (2345)  
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ctcaactatacg ggctcgagcg gcccgggggg caggtgaggg gagaggaggc ggcggcttag 120

ctgctacggg gtccggggcg gcccctccc gaggggggct caggaggagg aaggaggacc 180

cgtgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg ctg ctc 228  
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu Leu Leu  
1 5 10

tcc tgg gtg gca ggt ggt ttc ggg aac gca ggt gca agg cat cat 276  
Ser Trp Val Ala Gly Phe Gly Asn Ala Ala Ser Ala Arg His His  
14 19 24 29

cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt cac tat gga 324  
His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly  
30 35 40 45

act aaa ctg gcc tgc tac ggc tgg aga aga aac agc aag gga gtc 372  
Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val  
46 51 56 61

tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg gga 420  
Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly  
62 67 72 77

cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa acc tgc agt 468  
Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser  
78 83 88 93

caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac aga 516  
Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg  
94 99 104 109

tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc cac 564  
Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His  
110 115 120 125

atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc atg 612  
Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met  
126 131 136 141

ata aac tgt cag tac agc tgt gaa gac aca gaa gaa ggg cca cag tgc 660  
Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys  
142 147 152 157

ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga aga gac tgt 708  
Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys  
158 163 168 173

cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt ccc tac aat 756  
Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn  
174 179 184 189

cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa tgt cac att 804  
Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile  
190 195 200 205

ggg ttc gaa ctg caa tat atc agt gga cga tat gac tgt ata gat ata 852  
Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile  
206 211 216 221

aat gaa tgt act atg gat agc cat acg tgc agc cac cat gcc aat tgc 900  
Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys  
222 227 232 237

tcc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag gga tat aaa 948  
Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys  
238 243 248 253

ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct gtg aag gaa 996  
Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu  
254 259 264 269

gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag aag ttg ctt 1044  
Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu  
270 275 280 285

gct cac aaa aac agt atg aaa aag aag gca aaa att aaa aat gtt acc 1092  
Ala His Lys Asn Ser Met Lys Lys Ala Lys Ile Lys Asn Val Thr  
286 291 296 301

cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc ttc 1140  
Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe  
302 307 312 317

aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat gga ggt aaa 1188  
Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys  
318 323 328 333

aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat gag aaa aga 1236  
Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg  
334 339 344 349

gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc ctg cga gga 1284  
Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly  
350 355 360 365

gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc ggc ctg att 1332  
Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile  
366 371 376 381

ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat aaa gat tta	382	387	392	397	1380
Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu					
aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt gac tgg aaa	398	403	408	413	1428
Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys					
cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga gat aat	414	419	424	429	1476
Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn					
gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac aag aaa	430	435	440	445	1524
Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys					
gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc caa agc	446	451	456	461	1572
Asp Ile Gly Arg Leu Lys Leu Leu Pro Asp Leu Gln Pro Gln Ser					
aac ttc tgt ctc ttt gat tac cgg ctg gcc gga gac aaa gtc ggg	462	467	472	477	1620
Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly					
aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca tgg gag	478	483	488	493	1668
Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu					
aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa att cag ttg	494	499	504	509	1716
Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu					
tat caa gga act gat gct acc aaa agc atc att ttt gaa gca gaa cgt	510	515	520	525	1764
Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg					
ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc ttg ctt gtt	526	531	536	541	1812
Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val					
tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac tga atgttac	542	547	552	*	1861
Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp					
tatctttata tttgactttg tatgtcagtt ccctggtttt tttgatattg catcatagga					1921
cctctggcat tttagaatta ctagctaaaa aattgtaatg taccaacaga aatattattg					1981
taagatgcct ttcttgtata agatatgccat atatttgctt taaatatcat atcaactgtat					2041
cttctcagtc atttctgaat ctttccacat tatattataa aatatggaaa tgtcagttt					2101
tctccctcc tcagtatatc tgatttgtat aagtaagttg atgagcttct ctctacaaca					2161
tttcttagaaaa atagaaaaaaa aagcacagag aaatgtttaa ctgtttgact cttatgatac					2221
ttcttgaaaa ctatgacatc aaagatagac tttgcctaa gtggcttagc tgggtcttc					2281
atagccaaac ttgtatattt aaattctttg taataataat atccaaatca tcaaaaaaaa					2341
aaaaa					2345

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<210> 30
<211> 554
<212> PRT
<213> Homo sapiens

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Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg His His His Gly Leu
 20           25           30

Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr Gly Thr Lys Leu
 35           40           45

Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala
 50           55           60

Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys
 65           70           75           80

Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val
 85           90           95

Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn
100          105          110

Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met
115          120          125

Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys
130          135          140

Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro
145          150          155          160

Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile
165          170          175

Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys
180          185          190

Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu
195          200          205

Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys
210          215          220

Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr
225          230          235          240

Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
245          250          255

Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg
260          265          270

Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys
275          280          285

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Asn Ser Met Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro  
290 295 300

Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu  
305 310 315 320

Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn  
325 330 335

Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys  
340 345 350

Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe  
355 360 365

Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln  
370 375 380

Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser  
385 390 395 400

Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg  
405 410 415

Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly  
420 425 430

Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly  
435 440 445

Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys  
450 455 460

Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg  
465 470 475 480

Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr  
485 490 495

Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly  
500 505 510

Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly  
515 520 525

Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu  
530 535 540

Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
545 550

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<211> 2413  
<212> DNA  
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<220>  
<221> CDS  
<222> (258) .. (1922)

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acagcaccgg gtaactgcga gtggagcggagacggacccgagc ggctgaggag agaggaggcg 180  
gcggcttagc tgctacgggg tccggccggc gcctcccgaa ggggggctca ggaggaggaa 240  
ggaggacccg tgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg 290  
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu  
1 5 10  
ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg 338  
Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg  
15 20 25  
cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt cac tat 386  
His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr  
30 35 40  
gga act aaa ctg gcc tgc tgc tac ggc tgg aga aga aac agc aag gga 434  
Gly Thr Lys Leu Ala Cys Cys Tyr Gly Trp Arg Arg Asn Ser Lys Gly  
45 50 55  
gtc tgt gaa gct aca tgc gaa cct gga tgt aag ttt ggt gag tgc gtg 482  
Val Cys Glu Ala Thr Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val  
60 65 70 75  
gga cca aac aaa tgc aga tgc ttt cca gga tac acc ggg aaa acc tgc 530  
Gly Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys  
80 85 90  
agt caa gat gtg aat gag tgt gga atg aaa ccc cgg cca tgc caa cac 578  
Ser Gln Asp Val Asn Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His  
95 100 105  
aga tgt gtg aat aca cac gga agc tac aag tgc ttt tgc ctc agt ggc 626  
Arg Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly  
110 115 120  
cac atg ctc atg cca gat gct acg tgt gtg aac tct agg aca tgt gcc 674  
His Met Leu Met Pro Asp Ala Thr Cys Val Asn Ser Arg Thr Cys Ala  
125 130 135  
atg ata aac tgt cag tac agc tgt gaa gac aca gaa gaa ggg cca cag 722  
Met Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Glu Glu Gly Pro Gln  
140 145 150 155  
tgc ctg tgt cca tcc tca gga ctc cgc ctg gcc cca aat gga aga gac 770  
Cys Leu Cys Pro Ser Ser Gly Leu Arg Leu Ala Pro Asn Gly Arg Asp  
160 165 170  
tgt cta gat att gat gaa tgt gcc tct ggt aaa gtc atc tgt ccc tac 818  
Cys Leu Asp Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys Pro Tyr  
175 180 185  
aat cga aga tgt gtg aac aca ttt gga agc tac tac tgc aaa tgt cac 866  
Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His  
190 195 200  
att ggt ttc gaa ctg caa tat atc agt gga cga tat gac tgt ata gat 914  
Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Tyr Asp Cys Ile Asp  
205 210 215

ata aat gaa tgt act atg gat agc cat acg tgc agc cac cat gcc aat 962  
Ile Asn Glu Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn  
220 225 230 235

tgc ttc aat acc caa ggg tcc ttc aag tgt aaa tgc aag cag gga tat 1010  
Cys Phe Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr  
240 245 250

aaa ggc aat gga ctt cgg tgt tct gct atc cct gaa aat tct gtg aag 1058  
Lys Gly Asn Gly Leu Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys  
255 260 265

gaa gtc ctc aga gca cct ggt acc atc aaa gac aga atc aag aag ttg 1106  
Glu Val Leu Arg Ala Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu  
270 275 280

ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa aat gtt 1154  
Leu Ala His Lys Asn Ser Met Lys Lys Ala Lys Ile Lys Asn Val  
285 290 295

acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc 1202  
Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro  
300 305 310 315

ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat gga ggt 1250  
Phe Asn Tyr Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly  
320 325 330

aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat gag aaa 1298  
Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys  
335 340 345

aga gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc ctg cga 1346  
Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg  
350 355 360

gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc ggc ctg 1394  
Gly Asp Val Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu  
365 370 375

att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat aaa gca 1442  
Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala  
380 385 390 395

gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt gac 1490  
Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp  
400 405 410

tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga 1538  
Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg  
415 420 425

gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac 1586  
Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His  
430 435 440

aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc 1634  
Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Leu Pro Asp Leu Gln Pro  
445 450 455

caa agc aac ttc tgt ttg ctc ttt gat tac cgg ctg gcc gga gac aaa 1682  
Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys  
460 465 470 475

gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca 1730  
Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Asn Ala Leu Ala  
480 485 490

tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa att 1778  
Trp Glu Lys Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile  
495 500 505

cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa gca 1826  
Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala  
510 515 520

gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc ttg 1874  
Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu  
525 530 535

ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac tga 1922  
Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp  
540 545 550 555

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Cys Glu Pro Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys  
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His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
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Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu  
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Arg Cys Ser Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala  
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Pro Gly Thr Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn  
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Ser Met Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr  
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Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu  
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Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala  
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Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg  
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Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala Asp Leu Asn Ile Ser  
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Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His Lys Lys Asp Ile Gly  
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